IN THE CLAIMS:

Please amend claims 1, 17 and 52 as follows:

1. (Currently Amended) An isolated infectious chimeric respiratory syncytial virus (RSV) comprising a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a large polymerase protein (L), a M2 (ORF1) RNA polymerase elongation factor, and a partial or complete RSV genome or antigenome of one human RSV strain or subgroup virus combined with a heterologous gene or gene segment of a different human RSV strain or subgroup virus to form a chimeric RSV genome or antigenome encoding the infectious chimeric RSV.

2. (Previously Presented) The chimeric RSV of claim 1, wherein the chimeric genome or antigenome comprises a partial or complete human RSV genome or antigenome of one RSV subgroup or strain combined with a heterologous gene or gene segment from a different, human RSV subgroup.

3. (Previously Presented) The chimeric RSV of claim 2, wherein the heterologous gene or gene segment is from a human RSV subgroup A or human RSV subgroup B.

4. (Original) The chimeric RSV of claim 1, wherein the heterologous gene or gene segment is selected from a NS1, NS2, N, P, M, SH, M2(ORF1), M2(ORF2), L, F or G gene or gene segment.

5. (Original) The chimeric RSV of claim 4, wherein the heterologous gene or gene segment encodes a RSV F, G or SH glycoprotein or a cytoplasmic domain, transmembrane domain, ectodomain or immunogenic epitope thereof.

6. (Original) The chimeric RSV of claim 1, wherein the chimeric genome or antigenome comprises a partial or complete human RSV A subgroup genome or

antigenome combined with a heterologous gene or gene segment from a human RSV B subgroup virus.

7. (Original) The chimeric RSV of claim 6, wherein the heterologous gene or gene segment from human RSV B encodes a RSV F, G or SH glycoprotein or a cytoplasmic domain, transmembrane domain, ectodomain or immunogenic epitope thereof.

8. (Original) The chimeric RSV of claim 6, wherein one or more human RSV B subgroup glycoprotein genes F, G and SH or a cytoplasmic domain, transmembrane domain, ectodomain or immunogenic epitope thereof is substituted within a RSV A genome or antigenome.

9. (Original) The chimeric RSV of claim 8, wherein one or both human RSV B subgroup glycoprotein genes F and G is substituted to replace one or both counterpart F and G glycoprotein genes in the RSV A genome or antigenome.

10. (Original) The chimeric RSV of claim 9, wherein both human RSV B subgroup glycoprotein genes F and G are substituted to replace the counterpart F and G glycoprotein genes in the RSV A genome or antigenome.

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11. (Original) The chimeric RSV of claim 1, wherein a first heterologous gene or gene segment is substituted to replace a counterpart gene or gene segment within the partial or complete RSV genome or antigenome, and a second heterologous gene or gene segment is added to the partial or complete RSV genome or antigenome to form the chimeric RSV genome or antigenome.

12. (Original) The chimeric RSV of claim 1, wherein the chimeric genome or antigenome is further modified by one or more attenuating mutations.

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13. (Rejoined) The chimeric RSV of claim 12, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of attenuating mutations present within a panel of biologically derived mutant RSV strains, said panel comprising *cpts* RSV 248 (ATCC VR 2450), *cpts* RSV 248/404 (ATCC VR 2454), *cpts* RSV 248/955 (ATCC VR 2453), *cpts* RSV 530 (ATCC VR 2452), *cpts* RSV 530/1009 (ATCC VR 2451), *cpts* RSV 530/1030 (ATCC VR 2455), RSV B-1 *cp*52/2B5 (ATCC VR 2542), and RSV B-1 *cp*-23 (ATCC VR 2579).

14. (Rejoined) The chimeric RSV of claim 12, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of attenuating mutations specifying a temperature-sensitive amino acid substitution at Phe_{521}, Gln_{831}, Met_{1169} or Tyr_{1321} in the RSV polymerase gene L, or a temperature- sensitive nucleotide substitution in the gene-start sequence of gene M2.

15. (Rejoined) The chimeric RSV of claim 12, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of mutations from cold-passaged attenuated RSV, said complement of mutations including mutations specifying an amino acid substitution at Val_{267} in the RSV N gene, Glu_{218} or Thr_{523} in the RSV F gene, Cys_{319} or His_{1690} in the RSV polymerase gene L.

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16. (Original) The chimeric RSV of claim 1, wherein each of the human RSV B subgroup glycoprotein genes F and G is added or substituted within a human RSV A genome or antigenome to form the chimeric genome or antigenome, which is further modified to incorporate one or more attenuating mutations.

17. (Rejoined and Currently Amended) The chimeric RSV of claim 16, wherein both human RSV B subgroup glycoprotein genes F and G are substituted to replace counterpart F and G glycoprotein genes within an RSV A genome or antigenome to form the chimeric genome or antigenome, which is further modified to incorporate <u>one or more</u> attenuating point mutations selected from (i) a panel of mutations specifying temperature-sensitive amino acid substitutions at Gln_{831} and Tyr_{1321} in the RSV

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polymerase gene L; (ii) a temperature-sensitive nucleotide substitution in the gene-start sequence of gene M2; (iii) an attenuating panel of mutations adopted from cold-passaged RSV specifying amino acid substitutions Val_{267} Ile in the RSV N gene, and Cys_{319} to Tyr and His_{1690} Tyr in the RSV polymerase gene L; or (iv) a deletion of the SH gene.

18. (Original) The chimeric RSV of claim 12, wherein the chimeric genome or antigenome incorporates at least two attenuating mutations.

19. (Original) The chimeric RSV of claim 18, wherein the chimeric genome or antigenome incorporates attenuating mutations adopted from different biologically derived mutant RSV strains.

20. (Original) The chimeric RSV of claim 12, wherein the chimeric genome or antigenome includes at least one attenuating mutation stabilized by multiple nucleotide changes in a codon specifying the mutation.

21. (Original) The chimeric RSV of claim 1, formulated in a dose of 10^3 to 10^6 PFU of attenuated virus.

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22. (Rejoined) The chimeric RSV of claim 1 further comprising a nucleotide modification specifying a phenotypic change selected from a change in growth characteristics, attenuation, temperature-sensitivity, cold-adaptation, plaque size, host-range restriction, or a change in immunogenicity.

23. (Rejoined) The chimeric RSV of claim 22, wherein a SH, NS1, NS2, M2ORF2, or G gene is modified.

24. (Rejoined) The chimeric RSV of claim 23, wherein the SH, NS1, NS2, M2ORF2, or G gene is deleted in whole or in part or expression of the gene is ablated by introduction of one or more stop codons in an open reading frame of the gene.

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25. (Rejoined) The chimeric RSV of claim 22, wherein the nucleotide modification comprises a nucleotide deletion, insertion, substitution, addition or rearrangement of a cis-acting regulatory sequence of a selected RSV gene within the chimeric RSV genome or antigenome.

26. (Rejoined) The chimeric RSV of claim 25, wherein the cis-acting regulatory sequence of the selected RSV gene is changed to correspond to a heterologous regulatory sequence comprising a counterpart cis-acting regulatory sequence of the selected RSV gene from a different RSV subgroup or strain or a cis-acting regulatory sequence of a different RSV gene.

27. (Rejoined) The chimeric RSV of claim 25, wherein a gene end (GE) signal of the NS1 or NS2 gene is modified to correspond to the GE signal of the RSV N gene.

28. (Rejoined) The chimeric RSV of claim 22, wherein the nucleotide modification comprises an insertion, deletion, substitution, or rearrangement of a translational start site within the chimeric genome or antigenome.

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29. (Rejoined) The chimeric RSV of claim 28, wherein the translational start site for a secreted form of the RSV G glycoprotein is ablated.

30. (Rejoined) The chimeric RSV of claim 22, wherein the chimeric genome or antigenome is modified to encode a non-RSV molecule selected from a cytokine, a T-helper epitope, a restriction site marker, or a protein of a microbial pathogen capable of eliciting a protective immune response in a mammalian host.

31-34. (Cancelled)

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35. (Previously Presented) The chimeric RSV of claim 1 which is a complete virus.

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36-45. (Canceled)

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46. (Original) An immunogenic composition to elicit an immune response against RSV comprising an immunologically sufficient amount of the chimeric RSV of claim 1 in a physiologically acceptable carrier.

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47. (Original) The immunogenic composition of claim 46, formulated in a dose of 10^3 to 10^6 PFU.

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48. (Original) The immunogenic composition of claim 46, formulated for administration to the upper respiratory tract by spray, droplet or aerosol.

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49. (Original) The immunogenic composition of claim 46, wherein the chimeric RSV is a chimera of human RSV A and RSV B which elicits an immune response against either human RSV A or RSV B.

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50. (Original) The immunogenic composition of claim 46, wherein the chimeric RSV is a chimera of human RSV A and RSV B which elicits an immune response against both human RSV A and RSV B.

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37 32
51. (Original) The immunogenic composition of claim 46, wherein the chimeric RSV is a chimera of human RSV A and RSV B which elicits an immune response against either human RSV A or RSV B and wherein the composition further comprises an immunologically sufficient amount of a second attenuated RSV capable of eliciting an immune response against human RSV A or RSV B, whereby the composition elicits an immune response against both human RSV A or RSV B.

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52. (Currently Amended) An isolated polynucleotide molecule comprising a chimeric RSV genome or antigenome ~~which includes~~ encoding an infectious chimeric RSV, said isolated polynucleotide molecule including a partial or complete human RSV

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genome or antigenome of one RSV strain or subgroup virus combined with a heterologous gene or gene segment of a different human RSV strain or subgroup virus.

53. (Previously Presented) The isolated polynucleotide molecule of claim 52, wherein the chimeric genome or antigenome comprises a partial or complete human RSV genome or antigenome of one RSV subgroup combined with a heterologous gene or gene segment from a different, human RSV subgroup.

54. (Previously Presented) The isolated polynucleotide molecule of claim 52, wherein the heterologous gene or gene segment is from a human RSV subgroup A or human RSV subgroup B.

55. (Original) The isolated polynucleotide molecule of claim 52, wherein the heterologous gene or gene segment encodes a RSV F, G or SH glycoprotein or a cytoplasmic domain, transmembrane domain, ectodomain or immunogenic epitope thereof.

56. (Original) The isolated polynucleotide molecule of claim 52, wherein the chimeric genome or antigenome comprises a partial or complete human RSV A subgroup genome or antigenome combined with a heterologous gene or gene segment from a human RSV B subgroup virus.

57. (Original) The isolated polynucleotide molecule of claim 52, wherein one or both human RSV B subgroup glycoprotein genes F and G is substituted to replace one or both counterpart F and G glycoprotein genes in the RSV A genome or antigenome.

58. (Original) The isolated polynucleotide molecule of claim 57, wherein both human RSV B subgroup glycoprotein genes F and G are substituted to replace the counterpart F and G glycoprotein genes in the RSV A genome or antigenome.

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59. (Original) The isolated polynucleotide molecule of claim ~~52~~, wherein the chimeric genome or antigenome is further modified by one or more attenuating mutations.

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~~60~~. (Rejoined) The isolated polynucleotide molecule of claim ~~52~~, wherein both human RSV B subgroup glycoprotein genes F and G are substituted to replace counterpart F and G glycoprotein genes within an RSV A genome or antigenome to form the chimeric genome or antigenome, which is further modified to incorporate attenuating point mutations selected from (i) a panel of mutations specifying temperature-sensitive amino acid substitutions Gln_{831} to Leu and Tyr_{1321} to Asn in the RSV polymerase gene L; (ii) a temperature-sensitive nucleotide substitution in the gene-start sequence of gene M2; (iii) an attenuating panel of mutations adopted from cold-passaged RSV specifying amino acid substitutions Val_{267} Ile in the RSV N gene, and Cys_{319} to Tyr and His_{1690} Tyr in the RSV polymerase gene L; or (iv) a deletion of the SH gene.

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~~61~~. (Rejoined) The isolated polynucleotide molecule of claim ~~52~~, further comprising a nucleotide modification specifying a phenotypic change selected from a change in growth characteristics, attenuation, temperature-sensitivity, cold-adaptation, plaque size, host-range restriction, or a change in immunogenicity.

48 47
~~62~~. (Rejoined) The isolated polynucleotide molecule of claim ~~61~~, wherein a SH, NS1, NS2, M2ORF2, or G gene is modified.

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~~63~~. (Rejoined) The isolated polynucleotide molecule of claim ~~61~~, wherein the nucleotide modification comprises a nucleotide deletion, insertion, addition or rearrangement of a cis-acting regulatory sequence of a selected RSV gene within the chimeric RSV genome or antigenome.

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~~64~~. (Previously Presented) An expression vector for producing an infectious attenuated chimeric RSV comprising an isolated polynucleotide according to claim ~~52~~ operably linked with a transcriptional promoter and a transcriptional terminator.

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65. (Previously Presented) A host cell for producing an infectious attenuated chimeric RSV comprising a mammalian cell susceptible to RSV infection transfected or transformed with an expression vector according to claim 50 64.

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